**Fig. 1**

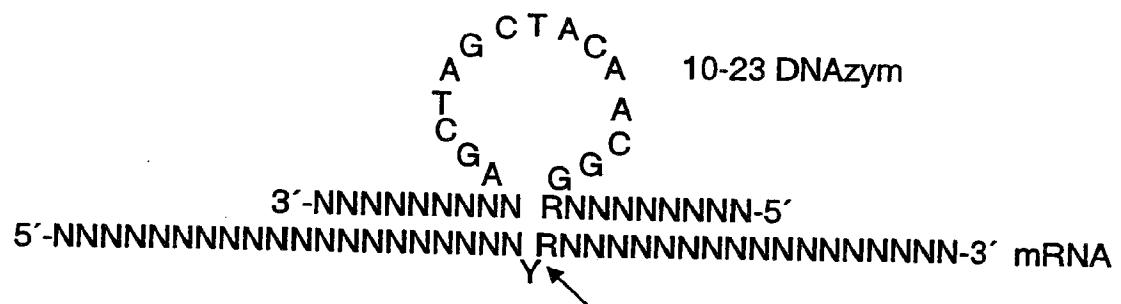


Fig. 2

Fig. 3

23593 (3-18)

10/574, 560

| Name | DNAzyme Sequenz |
|-------|---|
| hgd1 | 5' - TCGGTCAAGggctagctacaacgaTGCCTTGCT - 3' |
| hgd2 | 5' - GGCCTACGAGgctagctacaacgaCTGCTCGGT - 3' |
| hgd3 | 5' - GGCGGCGTAAggctagctacaacgaGACCTGCTC - 3' |
| hgd4 | 5' - CTCGGGTCAAggctagctacaacgaCTGGGTAGC - 3' |
| hgd5 | 5' - TCCTCTGCAAggctagctacaacgaCGGGGTCTT - 3' |
| hgd6 | 5' - ACTCTGCAAAGgctagctacaacgaTCTGCGAGC - 3' |
| hgd7 | 5' - GGGCGACGAGgctagctacaacgaTCTGCAATT - 3' |
| hgd8 | 5' - AAGGGGCGAAGgctagctacaacgaGACTCTGCA - 3' |
| hgd9 | 5' - AAAACGGGAAGgctagctacaacgaCAGGTTGTA - 3' |
| hgd10 | 5' - AGAATAAAAAGgctagctacaacgaGGGACCAGG - 3' |
| hgd11 | 5' - ATGGCAGAAAGgctagctacaacgaAAAACGGGA - 3' |
| hgd12 | 5' - AACTGGGTAAggctagctacaacgaGGCAGAATA - 3' |
| hgd13 | 5' - ATCCAAAAAAGgctagctacaacgaTGGGTATGG - 3' |
| hgd14 | 5' - AGGGGAAGAGggctagctacaacgaAAAAATCCA - 3' |
| hgd15 | 5' - TTTTAAAAAAGgctagctacaacgaTATCTTGGG - 3' |
| hgd16 | 5' - GTGGGGGGAGgctagctacaacgaGGGAAGGCT - 3' |
| hgd17 | 5' - GTTGAATGAGgctagctacaacgaTTGCTTTCG - 3' |
| hgd18 | 5' - GTCGTTGAAAGgctagctacaacgaGATTGCTT - 3' |
| hgd19 | 5' - GGCCCCGGAAGgctagctacaacgaCCGCCGCG - 3' |
| hgd20 | 5' - TCACCTCCAAGgctagctacaacgaGGCCTCGGC - 3' |
| hgd21 | 5' - CCGCCGTCAGgctagctacaacgaCTCCATGGC - 3' |
| hgd22 | 5' - GGTGGCTCAAggctagctacaacgaCCAGCGCGG - 3' |
| hgd23 | 5' - CGTTGAGCAGgctagctacaacgaGGCGGGGTG - 3' |
| hgd24 | 5' - CCGCGTCCAAGgctagctacaacgaGTAGGAGTG - 3' |
| hgd25 | 5' - CAGCGGGTAGgctagctacaacgaTGCGCCGCG - 3' |
| hgd26 | 5' - GCACATCCAAGgctagctacaacgaCTCCTCCGG - 3' |
| hgd27 | 5' - AAAAGCACAGgctagctacaacgaCCACCTCCT - 3' |
| hgd28 | 5' - TAAAAAGCAAGgctagctacaacgaATCCACCTC - 3' |
| hgd29 | 5' - GACCGTCGAGgctagctacaacgaGTTAAAAG - 3' |
| hgd30 | 5' - TTGCCTTGAGgctagctacaacgaCGTCGATGT - 3' |
| hgd31 | 5' - AGGGCGGGAGgctagctacaacgaGTGGTTGCC - 3' |
| hgd32 | 5' - TGGCCCTGAGgctagctacaacgaCGAGTTTCC - 3' |
| hgd33 | 5' - ACCTCTGCAAggctagctacaacgaCGTGGCCCT - 3' |
| hgd34 | 5' - CGGAGGGTAGgctagctacaacgactCTGCACC - 3' |
| hgd35 | 5' - GGCAGCACAGgctagctacaacgactGGCTCCC - 3' |
| hgd36 | 5' - CGGGCGGCCAGgctagctacaacgaACCTGGCTC - 3' |
| hgd37 | 5' - AGGGATCCAAGgctagctacaacgagaAGCAGAG - 3' |
| hgd38 | 5' - GGGTAGGGAGgctagctacaacgaccatGAAGC - 3' |
| hgd39 | 5' - GGGCTGAGAGgctagctacaacgaTCCAGGGGG - 3' |
| hgd40 | 5' - GTGGATGGAAGgctagctacaacgaGTCTTGGAG - 3' |
| hgd41 | 5' - CGTGGTGGAGgctagctacaacgaGGACGTCTT - 3' |
| hgd42 | 5' - GGGGGTAGAGgctagctacaacgaGGAGAGGGGG - 3' |
| hgd43 | 5' - GGAGGAGGAGgctagctacaacgaGAGGCCGGG - 3' |
| hgd44 | 5' - GCCCCCCCAGggctagctacaacgaAAGGAGGGAG - 3' |
| hgd45 | 5' - CCGGGGGAGAGgctagctacaacgaGTCTTCGG - 3' |
| hgd46 | 5' - GGACAGCGAAGgctagctacaacgaGGGTCCGGG - 3' |
| hgd47 | 5' - TGGGGTAGGAGgctagctacaacgaAGCGATGGG - 3' |
| hgd48 | 5' - CTTGAGGCAAGgctagctacaacgaTCTTCTCG - 3' |
| hgd49 | 5' - CACCTGGTAGgctagctacaacgaTTGAGGCAC - 3' |

Fig. 3 Cont.

| Name | DNAzyme Sequenz |
|-------|--|
| hgd50 | 5' -GCAGGGGCAggctagctacaacgaCTGGTACTT-3' |
| hgd51 | 5' -CCAGCTTCAGgctagctacaacgaGCTGTCGGG-3' |
| hgd52 | 5' -GTGGGACGAGgctagctacaacgaTCCAGCTTC-3' |
| hgd53 | 5' -GGAGTGGGAGgctagctacaacgaGACTCCAGC-3' |
| hgd54 | 5' -ATGCTGCCAGgctagctacaacgaGGGAGTGGG-3' |
| hgd55 | 5' -GGGCGGTCAggctagctacaacgaGCTGCCACG-3' |
| hgd56 | 5' -GAGGCTCCAGgctagctacaacgaCCAGGGCGG-3' |
| hgd57 | 5' -GTGGGTTCAGgctagctacaacgaGAGGAGGCT-3' |
| hgd58 | 5' -AGGTGGTGAGgctagctacaacgaGGGGTGGTG-3' |
| hgd59 | 5' -ACTCGGGCAggctagctacaacgaGTAGGGCGG-3' |
| hgd60 | 5' -GGAGCTGTAGgctagctacaacgaTCGGGCACG-3' |
| hgd61 | 5' -GGACTTGCAGgctagctacaacgaCCGAAGCCG-3' |
| hgd62 | 5' -GGGCCTGGAGgctagctacaacgaTTGCATCCG-3' |
| hgd63 | 5' -TGTGCTGGAGgctagctacaacgaCGGGCCTTG-3' |
| hgd64 | 5' -GTTCACACAGgctagctacaacgaTCCCTGCCT-3' |
| hgd65 | 5' -CAGTTCACAGgctagctacaacgaACTCCCTGC-3' |
| hgd66 | 5' -CACAGTTCAggctagctacaacgaACACTCCCT-3' |
| hgd67 | 5' -GTTGCCCAggctagctacaacgaAGTTCACAC-3' |
| hgd68 | 5' -TCGCCGCCAGgctagctacaacgaAGTGGGGTC-3' |
| hgd69 | 5' -CCCGTGCCAGgctagctacaacgaCTGCCGCC-3' |
| hgd70 | 5' -GGCGTTGCAGgctagctacaacgaAGGTAGTGT-3' |

Fig. 4

Multiple Sequence Alignments GATA-3

| | | | |
|-----------|------|--|------|
| Sequenz_1 | 1 | GGCGCCGTCTTGTAC TTTCAGAAAGAATGCATTCCCTGAAAAAAAAAAAAAAAGT | 60 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 1 | GGCGCCGTCTTGTAC TTTCAGAAAGAATGCATTCCCTGAAAAAAAAAAAAAAAGT | 60 |
| Sequenz_1 | 61 | AT-GAGAGCTGAGAGAGAGAGAGAGAGAGAGACGGAGGGAGAGCGAGACAGAGCG | 119 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 61 | ATGAGAGCTGAGAGAGAGAGAGAGAGAGACGGAGGGAGAGCGAGACAGAGCG | 120 |
| Sequenz_1 | 120 | AGCAACGCAATCTGAC CGAGCAGGTGCGTACGCCGCCGCTCCCTCCTCTGCTCTTC | 179 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 121 | AGCAACGCAATCTGAC CGAGCAGGTGCGTACGCCGCCGCTCCCTCCTCTGCTCTTC | 180 |
| Sequenz_1 | 180 | GCTACCCAGGTGACCC GAGGAGGGACTCCGCTCCGAGCGGCTGAGGACCCCGGTGCAGA | 239 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 181 | GCTACCCAGGTGACCC GAGGAGGGACTCCGCTCCGAGCGGCTGAGGACCCCGGTGCAGA | 240 |
| Sequenz_1 | 240 | GGAGCCTGGCTCGCAG AATTGCAGAGTCGTCGCCCTTTTACAACCTGGTCCCGTTTTA | 299 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 241 | GGAGCCTGGCTCGCAG AATTGCAGAGTCGTCGCCCTTTTACAACCTGGTCCCGTTTTA | 300 |
| Sequenz_1 | 300 | TTCTGCCATACCCAGT TTTTGGATTTGTCTTCCCTCTCTCTCTTGTCTAAACGACCC | 359 |
| Sequenz_2 | **** | ----- | **** |
| Sequenz_3 | 301 | TTCTGCCATACCCAGT TTTTGGATTTGTCTTCCCTCTCTCTTGTCTAAACGACCC | 360 |
| Sequenz_1 | 360 | CTCCAAGATAATTTT AAAAAACCTCTCCTTGCTCACCTTGCTTCCAGCCTTCCA | 419 |
| Sequenz_2 | 1 | ----- | 14 |
| Sequenz_3 | 361 | CTCCAAGATAATTTT AAAAAACCTCTCCTTGCTCACCTTGCTTCCAGCCTTCCA | 420 |
| Sequenz_1 | 420 | TCCCCCCCACCGAAAGC AAATCATTCAACGACCCCCGACCTTCCGACGGCAGGAGCCCCC | 479 |
| Sequenz_2 | 15 | TCCCCCCCACCGAAAGC AAATCATTCAACGACCCCCGACCTTCCGACGGCAGGAGCCCCC | 74 |
| Sequenz_3 | 421 | TCCCCCCCACCGAAAGC AAATCATTCAACGACCCCCGACCTTCCGACGGCAGGAGCCCCC | 480 |
| Sequenz_1 | 480 | GACCTCCCAGGCAGGAC CGCCCTTCCCGCGGGGTCCGGGCCCGCGAGAGGGC | 539 |
| Sequenz_2 | 75 | GACCTCCCAGGCAGGAC CGCCCTTCCCGCGGGGTCCGGGCCCGCGAGAGGGC | 133 |
| Sequenz_3 | 481 | GACCTCCCAGGCAGGAC CGCCCTTCCCGCGGGGTCCGGGCCCGCGAGAGGGC | 540 |
| Sequenz_1 | 540 | GCGAATACAGCCGAGG CCATGGAGGTGACGGCGGACAGCCCGCTGGGTGAGCCACAC | 599 |
| Sequenz_2 | 134 | GCGAATACAGCCGAGG CCATGGAGGTGACGGCGGACAGCCCGCTGGGTGAGCCACAC | 193 |
| Sequenz_3 | 541 | GCGAATACAGCCGAGG CCATGGAGGTGACGGCGGACAGCCCGCTGGGTGAGCCACAC | 600 |
| Sequenz_1 | 600 | CACCCCGCCGTGCTCA ACGGGCAGCACCCGGACACGCCACCCGGGCTCAGCCACTCC | 659 |
| Sequenz_2 | 194 | CACCCCGCCGTGCTCA ACGGGCAGCACCCGGACACGCCACCCGGGCTCAGCCACTCC | 253 |
| Sequenz_3 | 601 | CACCCCGCCGTGCTCA ACGGGCAGCACCCGGACACGCCACCCGGGCTCAGCCACTCC | 660 |
| Sequenz_1 | 660 | TACATGGACGGCGGCG AGTACCCGCTGCCGGAGGGAGGTGGATGTGCTTTAACATCGAC | 719 |
| Sequenz_2 | 254 | TACATGGACGGCGGCG AGTACCCGCTGCCGGAGGGAGGTGGATGTGCTTTAACATCGAC | 313 |
| Sequenz_3 | 661 | TACATGGACGGCGGCG AGTACCCGCTGCCGGAGGGAGGTGGATGTGCTTTAACATCGAC | 720 |
| Sequenz_1 | 720 | GGTCAAGGCACCCACG TCCC GCCCTACTACGGAAACTCGGTCAAGGCCACGGTGCAGAGG | 779 |
| Sequenz_2 | 314 | GGTCAAGGCACCCACG TCCC GCCCTACTACGGAAACTCGGTCAAGGCCACGGTGCAGAGG | 373 |
| Sequenz_3 | 721 | GGTCAAGGCACCCACG TCCC GCCCTACTACGGAAACTCGGTCAAGGCCACGGTGCAGAGG | 780 |
| Sequenz_1 | 780 | TACCCCTCCGACCCACC ACGGGAGCCAGGTGTGCCGCCGCCCTGCTCATGGATCCCTA | 839 |
| Sequenz_2 | 374 | TACCCCTCCGACCCACC ACGGGAGCCAGGTGTGCCGCCGCCCTGCTCATGGATCCCTA | 433 |
| Sequenz_3 | 781 | TACCCCTCCGACCCACC ACGGGAGCCAGGTGTGCCGCCGCCCTGCTCATGGATCCCTA | 840 |
| Sequenz_1 | 840 | CCCTGGCTGGACGGCG GCAAAGCCCTGGCAGCCACCAACCGCTCCCCCTGGAAATCTC | 899 |
| Sequenz_2 | 434 | CCCTGGCTGGACGGCG GCAAAGCCCTGGCAGCCACCAACCGCTCCCCCTGGAAATCTC | 493 |
| Sequenz_3 | 841 | CCCTGGCTGGACGGCG GCAAAGCCCTGGCAGCCACCAACCGCTCCCCCTGGAAATCTC hgd40 | 900 |
| Sequenz_1 | 900 | AGCCCCCTTCTCCAAAGA CGTCCATCCACCGGTCCCCGGCCCTCCGTCTACCCCC | 959 |
| Sequenz_2 | 494 | AGCCCCCTTCTCCAAAGA CGTCCATCCACCGGTCCCCGGCCCTCCGTCTACCCCC | 553 |
| Sequenz_3 | 901 | AGCCCCCTTCTCCAAAGA CGTCCATCCACCGGTCCCCGGCCCTCCGTCTACCCCC | 960 |
| Sequenz_1 | 960 | CCGGCCTCGTCCCTCCT CCTTGTGGGGGGCCACGGCAGCCCCGCACCTCTTCACCTTCCCG | 1019 |
| Sequenz_2 | 554 | CCGGCCTCGTCCCTCCT CCTTGTGGGGGGCCACGGCAGCCCCGCACCTCTTCACCTTCCCG | 613 |
| Sequenz_3 | 961 | CCGGCCTCGTCCCTCCT CCTTGTGGGGGGCCACGGCAGCCCCGCACCTCTTCACCTTCCCG | 1020 |
| Sequenz_1 | 1020 | CCCACCCCGCCGAAGG ACGTCTCCCCGGACCCATCGTGTCCACCCAGGCTCGGCCGGC | 1079 |
| Sequenz_2 | 614 | CCCACCCCGCCGAAGG ACGTCTCCCCGGACCCATCGTGTCCACCCAGGCTCGGCCGGC | 673 |
| Sequenz_3 | 1021 | CCCACCCCGCCGAAGG ACGTCTCCCCGGACCCATCGTGTCCACCCAGGCTCGGCCGGC | 1080 |

Fig. 4 Cont.

| | | | |
|-----------|------|--|------|
| Sequenz_1 | 1080 | TCGGCCCGGCAGGACG AGAAAGAGTGCCTCAAGTACCAAGCTGCCCTGCCCGACAGCATG | 1139 |
| Sequenz_2 | 674 | TCGGCCCGGCAGGACG AGAAAGAGTGCCTCAAGTACCAAGCTGCCCTGCCCGACAGCATG | 733 |
| Sequenz_3 | 1081 | TCGGCCCGGCAGGACG AGAAAGAGTGCCTCAAGTACCAAGCTGCCCTGCCCGACAGCATG | 1140 |
| Sequenz_1 | 1140 | AAGCTGGAGTCGTCCTACCTCCGGCAGCAGTACAGCTCCGGACTCTTC | 1199 |
| Sequenz_2 | 734 | AAGCTGGAGTCGTCCTACCTCCGGCAGCAGTACAGCTCCGGACTCTTC | 793 |
| Sequenz_3 | 1141 | AAGCTGGAGTCGTCCTACCTCCGGCAGCAGTACAGCTCCGGACTCTTC | 1200 |
| Sequenz_1 | 1200 | ACCCACCACCCCATCA CCACCTACCCGCCCTACGTGCCCGAGTACAGCTCCGGACTCTTC | 1259 |
| Sequenz_2 | 794 | ACCCACCACCCCATCA CCACCTACCCGCCCTACGTGCCCGAGTACAGCTCCGGACTCTTC | 853 |
| Sequenz_3 | 1201 | ACCCACCACCCCATCA CCACCTACCCGCCCTACGTGCCCGAGTACAGCTCCGGACTCTTC | 1260 |
| Sequenz_1 | 1260 | CCCCCCCAGCAGCCCTGC TGCGGGCTCCCCCACGGCTTGGATGCAAGTCCAGGCCAAG | 1319 |
| Sequenz_2 | 854 | CCCCCCCAGCAGCCCTGC TGCGGGCTCCCCCACGGCTTGGATGCAAGTCCAGGCCAAG | 913 |
| Sequenz_3 | 1261 | CCCCCCCAGCAGCCCTGC TGCGGGCTCCCCCACGGCTTGGATGCAAGTCCAGGCCAAG | 1320 |
| Sequenz_1 | 1320 | GCCCCGGTCCAGCACAG AAGGCAGGGAGTGTGAACGTGAGCTGTGGGCAACCTCGACCCACTG | 1379 |
| Sequenz_2 | 914 | GCCCCGGTCCAGCACAG ---GCAGGGAGTGTGAACGTGAGCTGTGGGCAACCTCGACCCACTG | 970 |
| Sequenz_3 | 1321 | GCCCCGGTCCAGCACAG AAGGCAGGGAGTGTGAACGTGAGCTGTGGGCAACCTCGACCCACTG | 1380 |
| Sequenz_1 | 1380 | TGGCGGCAGATGGCA CGGGACACTACCTGTGCAACGCCCTGGGGCTCTATCACAAAATG | 1439 |
| Sequenz_2 | 971 | TGGCGGCAGATGGCA CGGGACACTACCTGTGCAACGCCCTGGGGCTCTATCACAAAATG | 1030 |
| Sequenz_3 | 1381 | TGGCGGCAGATGGCA CGGGACACTACCTGTGCAACGCCCTGGGGCTCTATCACAAAATG | 1440 |
| Sequenz_1 | 1440 | AACGGACAGAACCCGGC CCCTCATTAGCCCCAACGCAAGGCTGTCTGCAGCCAGGAGAGCA | 1499 |
| Sequenz_2 | 1031 | AACGGACAGAACCCGGC CCCTCATTAGCCCCAACGCAAGGCTGTCTGCAGCCAGGAGAGCA | 1090 |
| Sequenz_3 | 1441 | AACGGACAGAACCCGGC CCCTCATTAGCCCCAACGCAAGGCTGTCTGCAGCCAGGAGAGCA | 1500 |
| Sequenz_1 | 1500 | GGGACGTCTGTGCGA ACTGTCA GACCCACCAACCCACACTCTGGAGGAGGAATGCCAAT | 1559 |
| Sequenz_2 | 1091 | GGGACGTCTGTGCGA ACTGTCA GACCCACCAACCCACACTCTGGAGGAGGAATGCCAAT | 1150 |
| Sequenz_3 | 1501 | GGGACGTCTGTGCGA ACTGTCA GACCCACCAACCCACACTCTGGAGGAGGAATGCCAAT | 1560 |
| Sequenz_1 | 1560 | GGGGACCCCTGTCTGCA ATGCCCTGGGGCTCTACTACAAGCTTCACAATATTAACAGACCC | 1619 |
| Sequenz_2 | 1151 | GGGGACCCCTGTCTGCA ATGCCCTGGGGCTCTACTACAAGCTTCACAATATTAACAGACCC | 1210 |
| Sequenz_3 | 1561 | GGGGACCCCTGTCTGCA ATGCCCTGGGGCTCTACTACAAGCTTCACAATATTAACAGACCC | 1620 |
| Sequenz_1 | 1620 | CTGACTATGAAGAAGGAAGGCATCCAGACCCAGAACCGAAAAATGTCTAGCAAATCAAA | 1679 |
| Sequenz_2 | 1211 | CTGACTATGAAGAAGGAAGGCATCCAGACCCAGAACCGAAAAATGTCTAGCAAATCAAA | 1270 |
| Sequenz_3 | 1621 | CTGACTATGAAGAAGGAAGGCATCCAGACCCAGAACCGAAAAATGTCTAGCAAATCAAA | 1680 |
| Sequenz_1 | 1680 | AAGTGCAAAAAAAGTCATGACTCACTGGAGGACTTCCCCAACAACAGCTCGTTAACCG | 1739 |
| Sequenz_2 | 1271 | AAGTGCAAAAAAAGTCATGACTCACTGGAGGACTTCCCCAACAACAGCTCGTTAACCG | 1330 |
| Sequenz_3 | 1681 | AAGTGCAAAAAAAGTCATGACTCACTGGAGGACTTCCCCAACAACAGCTCGTTAACCG | 1740 |
| Sequenz_1 | 1740 | GCCGCCCTCTCCAGAC ACATGTCTCCCTGAGCCACATCTGCCCTTCAGCCACCCAGC | 1799 |
| Sequenz_2 | 1331 | GCCGCCCTCTCCAGAC ACATGTCTCCCTGAGCCACATCTGCCCTTCAGCCACCCAGC | 1390 |
| Sequenz_3 | 1741 | GCCGCCCTCTCCAGAC ACATGTCTCCCTGAGCCACATCTGCCCTTCAGCCACCCAGC | 1800 |
| Sequenz_1 | 1800 | CACATGCTGACCACGC CCACGCCGATGCACCCGCCATCCAGCCTGTCTTTGGACCACAC | 1859 |
| Sequenz_2 | 1391 | CACATGCTGACCACGC CCACGCCGATGCACCCGCCATCCAGCCTGTCTTTGGACCACAC | 1450 |
| Sequenz_3 | 1801 | CACATGCTGACCACGC CCACGCCGATGCACCCGCCATCCAGCCTGTCTTTGGACCACAC | 1860 |
| Sequenz_1 | 1860 | CACCCCTCCAGCATGG TCACCGCCATGGGTTAGAGCCCTGCTCGATGCTCACAGGGCCCC | 1919 |
| Sequenz_2 | 1451 | CACCCCTCCAGCATGG TCACCGCCATGGGTTAGAGCCCTGCTCGATGCTCACAGGGCCCC | 1510 |
| Sequenz_3 | 1861 | CACCCCTCCAGCATGG TCACCGCCATGGGTTAGAGCCCTGCTCGATGCTCACAGGGCCCC | 1920 |
| Sequenz_1 | 1920 | CAGCGAGAGTCCCTGC AGTCCCTTCGACTTGCAATTGGCAGGAGCAGTATCATGAAGC | 1979 |
| Sequenz_2 | 1511 | CAGCGAGAGTCCCTGC AGTCCCTTCGACTTGCAATTGGCAGGAGCAGTATCATGAAGC | 1570 |
| Sequenz_3 | 1921 | CAGCGAGAGTCCCTGC AGTCCCTTCGACTTGCAATTGGCAGGAGCAGTATCATGAAGC | 1980 |
| Sequenz_1 | 1980 | CTAAACGCGATGGATA TATGTTTTGAAGGCAGAAAGCAAATTATGCTTGGCCACTTTG | 2039 |
| Sequenz_2 | 1571 | CTAAACGCGATGGATA TATGTTTTGAAGGCAGAAAGCAAATTATGCTTGGCCACTTTG | 1630 |
| Sequenz_3 | 1981 | CTAAACGCGATGGATA TATGTTTTGAAGGCAGAAAGCAAATTATGCTTGGCCACTTTG | 2040 |
| Sequenz_1 | 2040 | AAAGGAGGCTCACTGTG TGCTGTGTTCCAACCACGTGAATCTGGACCCCATCTGTGAATA | 2099 |
| Sequenz_2 | 1631 | AAAGGAGGCTCACTGTG TGCTGTGTTCCAACCACGTGAATCTGGACCCCATCTGTGAATA | 1690 |
| Sequenz_3 | 2041 | AAAGGAGGCTCACTGTG TGCTGTGTTCCAACCACGTGAATCTGGACCCCATCTGTGAATA | 2100 |

Fig. 4 Cont.

| | | | |
|-----------|------|--|------|
| Sequenz_1 | 2100 | AGCCATTCTGACTCAT ATCCCCTATTAAACAGGGTCTCTAGTGCTGTGAAAAA-T | 2158 |
| Sequenz_2 | 1691 | AGCCATTCTGACTCAT ATCCCCTATTAAACAGGGTCTCTAGTGCTGTGAAAAAAT | 1750 |
| Sequenz_3 | 2101 | AGCCATTCTGACTCAT ATCCCCTATTAAACAGGGTCTCTAGTGCTGTGAAAAAAT | 2160 |
| Sequenz_1 | 2159 | CTGAACATTGCATATACTTATATTGTAAGAAATACTGTACAATGACTTATTGCATCT | 2218 |
| Sequenz_2 | 1751 | CTGAACATTGCATATACTTATATTGTAAGAAATACTGTACAATGACTTATTGCATCT | 1810 |
| Sequenz_3 | 2161 | CTGAACATTGCATATACTTATATTGTAAGAAATACTGTACAATGACTTATTGCATCT | 2220 |
| Sequenz_1 | 2219 | GGGTAGCTGTAAGGCA TGAAGGATGCCAAGAAGTTAAGGAATATGGGAGAAATAGTGTG | 2278 |
| Sequenz_2 | 1811 | GGGTAGCTGTAAGGCA TGAAGGATGCCAAGAAGTTAAGGAATATGGGAGAAATAGTGTG | 1870 |
| Sequenz_3 | 2221 | GGGTAGCTGTAAGGCA TGAAGGATGCCAAGAAGTTAAGGAATATGGGAGAAATAGTGTG | 2280 |
| Sequenz_1 | 2279 | GAAATTAAAGAAGAAC TAGGTCGATATTCAAATGGACAAACTGCCAGTTTGTTCCTT | 2338 |
| Sequenz_2 | 1871 | GAAATTAAAGAAGAAC TAGGTCGATATTCAAATGGACAAACTGCCAGTTTGTTCCTT | 1930 |
| Sequenz_3 | 2281 | GAAATTAAAGAAGAAC TAGGTCGATATTCAAATGGACAAACTGCCAGTTTGTTCCTT | 2340 |
| Sequenz_1 | 2339 | TCACTGGCCACAGTTG TTTGATGCATTAAAAGAAAATAAAAAGAAAAAGAGAAAAG | 2398 |
| Sequenz_2 | 1931 | TCACTGGCCACAGTTG TTTGATGCATTAAAAGAAAATAAAAAGAAAAAGAGAAAAG | 1990 |
| Sequenz_3 | 2341 | TCACTGGCCACAGTTG TTTGATGCATTAAAAGAAAATAAAAAGAAAA-GAGAAAAG | 2399 |
| Sequenz_1 | 2399 | A----- | 2399 |
| Sequenz_2 | 1991 | AAAAAAAAGAAAAAA GTTGTAGGCGAATCATTGTTCAAAGCTGTTGCCCTCTGCAA | 2050 |
| Sequenz_3 | 2400 | AAAAAAAAGAAAAAA GTTGTAGGCGAATCATTGTTCAAAGCTGTTGCC-TCTGCAA | 2458 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2051 | GGAAATACCACTCTG GGCAATCAGTGTACCGTTACCGTACCAAGTTGCCATTGAGGGTTTCAG | 2110 |
| Sequenz_3 | 2459 | GGAAATACCACTCTG GGCAATCAGTGTACCGTTACCGTACCAAGTTGCCATTGAGGGTTTCAG | 2518 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2111 | AGAGCCTTTCTAGG CCTACATGTTGTGAACAAGTCCCTGTAATTGTTGTTGTATG | 2170 |
| Sequenz_3 | 2519 | AGAGCCTTTCTAGG CCTACATGTTGTGAACAAGTCCCTGTAATTGTTGTTGTATG | 2578 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2171 | TATAATTCAAAGCACC AAAATAAGAAAAGATGTAGATTATTCATCATATTACAGAC | 2230 |
| Sequenz_3 | 2579 | TATAATTCAAAGCACC AAAATAAGAAAAGATGTAGATTATTCATCATATTACAGAC | 2638 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2231 | CGAACTGTTGTATAAA TTTATTTACTGCTAGCTTAAGAACTGCTTCTTCGTTGTT | 2290 |
| Sequenz_3 | 2639 | CGAACTGTTGTATAAA TTTATTTACTGCTAGCTTAAGAACTGCTTCTTCGTTGTT | 2698 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2291 | GTTTCAATATTTCTCTCTCAATTTCGGTTGAATAACTAGATTACATTCAAGTTG | 2350 |
| Sequenz_3 | 2699 | GTTTCAATATTTCTCTCTCAATTTCGG----- | 2731 |
| Sequenz_1 | **** | ----- | **** |
| Sequenz_2 | 2351 | GCAAAAAAAAAA | 2365 |
| Sequenz_3 | **** | ----- | **** |

GGCGCCGTCTGATACTTTAGAAAGAATGCATCCCTGTAAAAAAAAAA
 AAAAAAAAATACTGAGAGAGGGAGAGAGAGAGAGAGAGACCGG
 AGGGAGAGCGAGACAGAGCGAGCAACGCAATCTGACCGAGCAGGTCGTAC
 GCCGCCGCTCCTCCTCTCTGCTTCTGCTACCCAGGTGACCCGAGG
 AGGGACTCCGCCTCCGAGCGGCTGAGGACCCGGTGCAGAGGAGCCTGGC
 TCGCAGAATTGCAAGAGTCGTCGCCCTTTTACAACCTGGTCCCGTTTA
 TTCTGCCATACCCAGTTTGGATTTGTCTTCCCCTCTTCTTTGC
 TAAACGACCCCTCCAAGATAATTAAAACCTTCTCCTTGCTCACC
 TTTGCTCCAGCCTCCCATCCCCCACCGAAAGCAAATCATTCAACGA
 CCCCCGACCCCTCCGACGGCAGGAGCCCCCGACCTCCAGGCGGACGCC
 CTCCCTCCCCGCGCGGGTTCCGGGCCGGCAGAGGGCGCAGCACAG
 CCGAGGCCATGGAGGTGACGGCGGACCAGCCGCGCTGGGTGAGCCACCC
 CACCCCGCGTGCCTCAACGGCAGCACCGACCGACCCGGCT
 CAGCCACTCCTACATGGACGCGGCGCAGTACCCGCTGCCGGAGGGAGGTGG
 ATGTGCTTTAACTCGACGGTCAAGGCAACCACGTCCCGCCCTACTAC
 GGAAACTCGGTCAAGGCCACGGTGCAGAGGTACCCCTCCGACCCACCG
 GAGCCAGGTGTGCCGCCGCTCTGCTCATGGATCCCTACCCGGCTGG
 ACGGCCGCAAAGCCCTGGCAGCCACACCGCCTCCCCCTGGAATCTC
 AGCCCCCTCTCCAAGACGTCCATCCACCAAGGCTCCCCGGGCCCTCTC
 CGTCTACCCCCCGGCCCTCGTCTCCTCTGTCGGGGGCCACGCCAGCC
 CGCACCTCTCACCTCCGCCACCCCGCGAAGGACGTCTCCCCGGAC
 CCATCGCTGTCCACCCAGGCTCGGCCGGCTCGGCCGGCAGGACGAGAA
 AGAGTGCTCAAGTACCAAGGTGCCCTGCCCCGACAGCATGAAGCTGGAGT
 CGTCCCACCTCCGTGGCAGCATGACCGCCCTGGGTGGAGCCTCTCG
 ACCCACCAACCCATCACCAACCTACCGCCCTACGTGCCAGTACAGCTC
 CGGACTCTCCCCCCCAGCAGCCTGCTGGCGCTCCCCCACCGGCTTCG
 GATGCAAGTCCAGGCCAAGGCCCGGTCCAGCACAGAAGGCAGGGAGTGT
 GTGAACGTGGGGCAACCTCGACCCACTGTGGCGCGAGATGGCACGGG
 ACACTACCTGTGCAACGCCCTGGGCTCTAACAAAAGAACGGACAGA
 ACCGGCCCTCTTAAGCCAAGCGAAGGCTCTGAGCCAGGAGAGCA
 GGGACTCTGGCAACTCTCAGACCACCAACACTCTGGAGGAG
 GAACTGCAAGGGGACCTCTGCACTGGCTCTACTACAAGC
 TTCACACCTTAACAGACCCCTGACTGAAGAAGGAAGGCTCCAGACC
 AGAAACCGAAAACTAGCAAACCAAAAGCAAAAGCAGAAGGAGA
 CTCACGGGACTCTCCAAGAACAGCTCTTAACCCGGCCGCCCTCT
 CCAGACACCTCCCTGAGCCACTCGCCCTTCAGCCACCCAGC
 CACGCTGACCAAGCCCACGCCGAGCACCCGCCCTCCAGC
 TGGACCAACCACCCCTCCAGGCTGACCCGCGCTGGTAGAGCCCTG
 CTCGAGCTCACAGGGCCCCCAGCGAGACCCCTGCAACCCCTTCGACT
 TGCCTTTGCAAGGAGCACTGCAAGGCTAAACCGGAGGAGA
 TTTTGAAGGAGAAAGCAAAATCTGCTGCCACTTGCAAAAGGAGCTC
 ACTGCTCTCTCTCCAAACCACTGAACTGGACCCCTGAGCTGAA
 AGCCCTCTGACTCTACCCCTTTAACAGGCTCTAGCTGCTGAA
 AAAAAAAAGCTGAACATGCAAAACTTAAAGAAAGAAACTCT
 ACAAGACTTTATGCACTGGTAGCTAAAGGAGGAAGGAGGAGCAAG
 AAGTTAACAGGAAAGGGAGAAAGGAATTAAGAAGAAACTAG
 CTGAACTCAAGGGACAAACTGCCATTGCTTCCCTTCACTGGCCA
 CAGCTCTTGCTGCTAAAGAAAGAAAAAGAAAAAGAGAAAAGA
 AAAAAAAAGAAAAAAATCTAGGCGACCTCTGCTCAAAGCTCTGGCC
 TCTGCAAAGGAAAGCCAGCTCTGGCAACAGCTTACCTCTCACCACT
 TGCCAGGCTTCAGAGAGCCTTTCTAGGCTTACCTGCTTCTGAA
 ACAACCCCTTAACTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTG
 AGAAAAGCTAGAACTTCTGCTCAAAGGAGCAACTCTGCTTCTG
 TAACTTACTGCTACTTAAGAAACTGCTTCTTCTGCTTCTGCTTCTG
 TTCATTTCTCTCTCTCACTTTC

Fig. 4 A

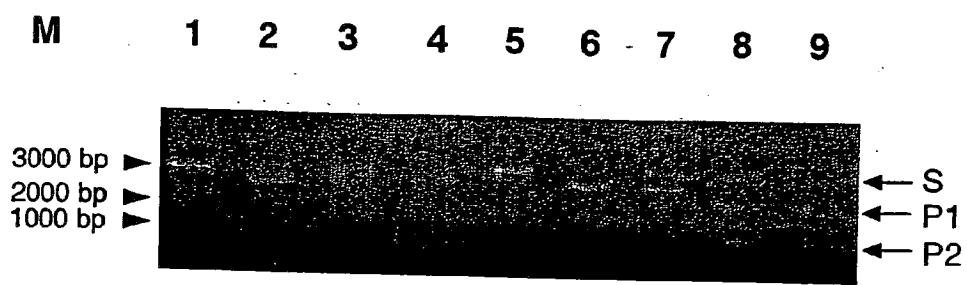


Fig. 5

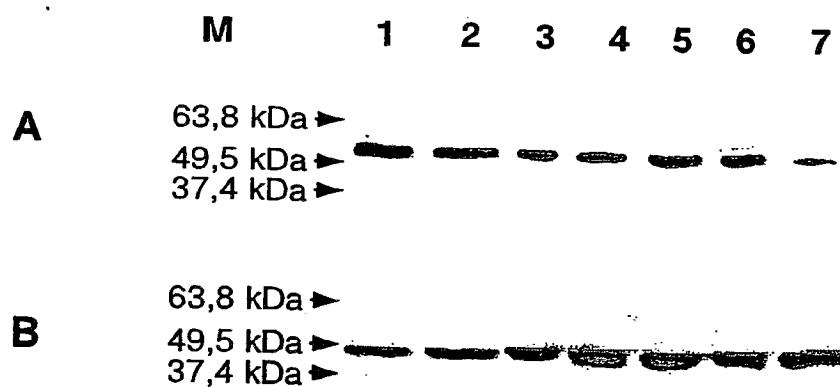


Fig. 6

Fig. 7

| Name | DNAzyme Sequenz |
|------|-------------------------------------|
| td1 | TGGCTTCTAaggctagctacaacgaGCCCTCGTC |
| td2 | GGGCTCTGAggctagctacaacgaGCCTGGCTT |
| td3 | GGGACCCCCAggctagctacaacgaCGGAGCCCCG |
| td4 | GGTGGGGGAggctagctacaacgaCCCACCGGA |
| td5 | GGCGGGGGAggctagctacaacgaCCGAGGGCC |
| td6 | GGGCTGGGAggctagctacaacgaGGGCAGGGA |
| td7 | CGTCGAGGAggctagctacaacgaCCGCCCCTC |
| td8 | GGGCTGGCAggctagctacaacgaCTTCCCFTA |
| td9 | CGATGCCCAggctagctacaacgaCCGGGGCGG |
| td10 | GCTCCACGAggctagctacaacgaGCCCATCCG |
| td11 | CCGGCTCCAggctagctacaacgaGATGCCAT |
| td12 | TCTCCGCAAggctagctacaacgaCCGGCTCCA |
| td13 | CCGTCAGCAGgctagctacaacgaGTCTCCGCA |
| td14 | TCCCCGGCAggctagctacaacgaCGGCTCGGT |
| td15 | CCCCCGCGAggctagctacaacgaGCTCGTCCG |
| td16 | GTAGGGAGGAggctagctacaacgaCCCAGGCTG |
| td17 | GGGCGGGCAggctagctacaacgaCAAGGCGCC |
| td18 | CGGGAAGGAGgctagctacaacgaTCGCCCCG |
| td19 | TAGTCCTCAggctagctacaacgaGCGGCCCCG |
| td20 | TCCCCGACAggctagctacaacgaCTCCAGTCC |
| td21 | TTTCCCCGAggctagctacaacgaACCTCCAGT |
| td22 | TGAGCGCGAggctagctacaacgaCCTCAGTTT |
| td23 | GGACCACAAggctagctacaacgaAGGTGGTTG |
| td24 | CTTGGACCAGgctagctacaacgaAACAGGTGG |
| td25 | AAACTTGGAGgctagctacaacgaCACAAACAGG |
| td26 | CTGATTAAAggctagctacaacgaTTGGACCAC |
| td27 | TGGTGCTGAggctagctacaacgaAAACTTGG |
| td28 | TGATGATCAGgctagctacaacgaCTCTGTCTG |
| td29 | TGGTGATGAggctagctacaacgaCATCTCTGT |
| td30 | GCTTGGTGAggctagctacaacgaGATCATCTC |
| td31 | ATGGGAACAggctagctacaacgaCCGCCGTCC |
| td32 | GAATGGGAAGgctagctacaacgaATCCGCCGT |
| td33 | TGACAGGAAAggctagctacaacgaGGGAACATC |
| td34 | AGTAAATGAggctagctacaacgaAGGAATGGG |
| td35 | CACAGTAAAggctagctacaacgaGACAGGAAT |
| td36 | GCCCCGCCAggctagctacaacgaAGTAAATGA |
| td37 | CCACAAACAggctagctacaacgaCCTGTAGTG |
| td38 | GTCCACAAAggctagctacaacgaATCCTGTAG |
| td39 | CCACGTCCAggctagctacaacgaAAACATCCT |
| td40 | CCAAGACCAGgctagctacaacgaGTCCACAAA |
| td41 | CCACCAAGAggctagctacaacgaCACGTCCAC |
| td42 | GCTGGTCCAggctagctacaacgaCAAGACCAC |
| td43 | GCTCTGGTAggctagctacaacgaCGCCAGTGG |
| td44 | CTGCACCCAggctagctacaacgaTTGCCGCTC |
| td45 | CACACTGCAggctagctacaacgaCCACTTGCC |
| td46 | CTTTCCACAggctagctacaacgaTGCACCCAC |
| td47 | GCCTTTCCAggctagctacaacgaACTGCACCC |
| td48 | TTCCTGGCAggctagctacaacgaGCTGCCCTC |

Fig. 7 Cont.

| Name | DNAzyme Sequenz |
|------|------------------------------------|
| TD49 | GTTGGACGTAGgctagctacaacgaAGGCGGTTT |
| TD50 | CCGGGTGGAGgctagctacaacgaGTACAGGGCG |
| TD51 | CCTGGCGCAggctagctacaacgaCCAGTGCAC |
| TD52 | CAAATGAAAGgctagctacaacgaTTCCTGGCG |
| TD53 | TTTCCCAAAGgctagctacaacgaGAAACTTCC |
| TD54 | ATTGTTGGAGgctagctacaacgaGCCCCCTTG |
| TD55 | TGGGTACACAggctagctacaacgaTGTTGGACG |
| TD56 | TCTGGGTCAggctagctacaacgaATTGTTGGA |
| TD57 | GCACAATCAAggctagctacaacgaCTGGGTAC |
| TD58 | GGAGCACAAggctagctacaacgaCATCTGGGT |
| TD59 | ACTGGAGCAggctagctacaacgaAATCATCTG |
| TD60 | ATGGAGGGAGgctagctacaacgaTGGAGCACA |
| TD61 | TGGTACTTAggctagctacaacgaGGAGGGACT |
| TD62 | GGGCTGGTAggctagctacaacgaTTATGGAGG |
| TD63 | TCAACGATAggctagctacaacgaGCAGCCGGG |
| TD64 | CCTCAACGAggctagctacaacgaATGCAGCCG |
| TD65 | TCACCTCAAggctagctacaacgaGATATGCAG |
| TD66 | CGTCGTTCAggctagctacaacgaCTCAACGAT |
| TD67 | GTAAAGATAggctagctacaacgaGCGTGTG |
| TD68 | AAGTAAAGAGgctagctacaacgaATGCGTGT |
| TD69 | GGCAATGAAggctagctacaacgaTGGGTTTCT |
| TD70 | TCACGGCAAggctagctacaacgaGAAGTGGGT |
| TD71 | AGGCAGTCAggctagctacaacgaGGCAATGAA |
| TD72 | ATCTCGGCAggctagctacaacgaTCTGGTAGG |
| TD73 | GCTGAGTAAggctagctacaacgaCTCGGCATT |
| TD74 | TATTATCAAggctagctacaacgaTTTCAGCTG |
| TD75 | GGGTTATTAGgctagctacaacgaCAATTTCA |
| TD76 | AAGGGGTTAggctagctacaacgaTATCAATT |
| TD77 | CTCCCGGAAGgctagctacaacgaCCTTGCGA |
| TD78 | GTACATGGAGgctagctacaacgaTCAAAGTTC |

Multiple Sequenz Alignments T-bet

| | | | |
|-------|------|---|------|
| Seq_1 | 1 | CGGCCCCGCTGGAGAGGAAGGCCGAGAGCTGCCGCCGCTGCCGGACGAGGGCGTAGAAG | 60 |
| Seq_2 | 1 | CGGCCCCGCTGGAGAGGAAGGCCGAGAGCTGCCGCCGCTGCCGGACGAGGGCGTAGAAG | 60 |
| Seq_1 | 61 | CCAGGCCTCAGAGCCCAGGGCTCCGGTGGGTCCCCCACCCGGCCCTGGGTCCCCGCC | 120 |
| Seq_2 | 61 | CCAGGCCTCAGAGCCCAGGGCTCCGGTGGGTCCCCCACCCGGCCCTGGGTCCCCGCC | 120 |
| Seq_1 | 121 | CCTGCTCCCTGCCATCCAGGCCACCGGACCCCTCTCGCGCCCGAGGGGGGGTCCCTCG | 180 |
| Seq_2 | 121 | CCTGCTCCCTGCCATCCAGGCCACCGGACCCCTCTCGCGCCGGAGGGGGGGTCCCTCG | 180 |
| Seq_1 | 181 | ACGGCTACGGGAAGGTGCCAGCCCAGGGATGGGCATCGTGGAGGCCGGTTGCGGAGA | 240 |
| Seq_2 | 181 | ACGGCTACGGGAAGGTGCCAGCCCAGGGATGGGCATCGTGGAGGCCGGTTGCGGAGA | 240 |
| Seq_1 | 241 | CATGCTGACGGGACCCGAGCCGATGCCGGGAGCGACGGAGGGCCGGCGCCTGGCGCGA | 300 |
| Seq_2 | 241 | CATGCTGACGGGACCCGAGCCGATGCCGGGAGCGACGGAGGGCCGGCGCCTGGCGCGA | 300 |
| Seq_1 | 301 | CCCGCAGCACTGCTACTTCTACCCGGAGCCGGCGCAGGACGCGGACGACCGTCGCGG | 360 |
| Seq_2 | 301 | CCCGCAGCACTGCTACTTCTACCCGGAGCCGGCGCAGGACGCGGACGACCGTCGCGG | 360 |
| Seq_1 | 361 | GGGCGGCAGCCTGGGTCTCCCTACCCGGGGGGCGCCTTGGTGCCCGCCCCCGAGCCG | 420 |
| Seq_2 | 361 | GGGCGGCAGCCTGGGTCTCCCTACCCGGGGGGCGCCTTGGTGCCCGCCCCCGAGCCG | 420 |
| Seq_1 | 421 | CTTCCTTGGAGCCTACGCCCTACCCGCCGACCCCAAGCGGCCGGCTTCCCCGGCGGG | 480 |
| Seq_2 | 421 | CTTCCTTGGAGCCTACGCCCTACCCGCCGACCCCAAGCGGCCGGCTTCCCCGGCGGG | 480 |
| Seq_1 | 481 | CGAGTCCTTCCCAGCCGGACGCCGAGGGCTACCGAGCCGGAGGGCTACGCCGC | 540 |
| Seq_2 | 481 | CGAGTCCTTCCCAGCCGGACGCCGAGGGCTACCGAGCCGGAGGGCTACGCCGC | 540 |
| Seq_1 | 541 | CCCGGACCCCGCGCGCCGGCTCTACCCGGGGCCCGTGAGGACTACCGCTACCCGGGG | 600 |
| Seq_2 | 541 | CCCGGACCCCGCGCGCCGGCTCTACCCGGGGCCCGTGAGGACTACCGCTACCCGGGG | 600 |
| Seq_1 | 601 | ACTGGAGGTGTCGGGAAACTGAGGGTGCCTCAACAACCACCTGTTGTGGTCCAAGTT | 660 |
| Seq_2 | 601 | ACTGGAGGTGTCGGGAAACTGAGGGTGCCTCAACAACCACCTGTTGTGGTCCAAGTT | 660 |
| Seq_1 | 661 | TAATCAGCACCAGACAGAGATGATCATACCAAGCAGGGACGGCGATGTTCCCATTCCT | 720 |
| Seq_2 | 661 | TAATCAGCACCAGACAGAGATGATCATACCAAGCAGGGACGGCGATGTTCCCATTCCT | 720 |
| Seq_1 | 721 | GTCATTTACTGTGGCCGGCTGGAGCCACCAAGCCACTACAGGATGTTGTGGACGTGGT | 780 |
| Seq_2 | 721 | GTCATTTACTGTGGCCGGCTGGAGCCACCAAGCCACTACAGGATGTTGTGGACGTGGT | 780 |
| Seq_1 | 781 | CTTGGTGGACCAGCACCACGGCTTACAGAGCGGCAAGTGGGTGCAGTGTGGAAAGGC | 840 |
| Seq_2 | 781 | CTTGGTGGACCAGCACCACGGCTTACAGAGCGGCAAGTGGGTGCAGTGTGGAAAGGC | 840 |
| Seq_1 | 841 | CGAGGGCAGCATGCCAGGAACCGCCTGTACGCCACCCGACTCCCCAACACAGGAGC | 900 |
| Seq_2 | 841 | CGAGGGCAGCATGCCAGGAACCGCCTGTACGCCACCCGACTCCCCAACACAGGAGC | 900 |
| Seq_1 | 901 | GCACGTGGATGCCAGGAAGTTTCACTGGAAACTAAAGCTCACAAACAAAGGGGGC | td54 |
| Seq_2 | 901 | GCACGTGGATGCCAGGAAGTTTCACTGGAAACTAAAGCTCACAAACAAAGGGGGC | 960 |
| Seq_1 | 961 | GTGACCCAGATGATTGTGCTCCAGTCCCTCCATAAGTACCGCCGGCT | 1020 |
| Seq_2 | 961 | GTCCAACATGTGACCCAGATGATTGTGCTCCAGTCCCTCCATAAGTACCGCCGGCT | 1020 |
| Seq_1 | 1021 | GCATATCGTGGAGGTGAACGACGGAGAGGCCAGAGGCCAGCGCTGCAACGCTTCCAACACGCA | 1080 |
| Seq_2 | 1021 | GCATATCGTGGAGGTGAACGACGGAGAGGCCAGAGGCCAGCGCTGCAACGCTTCCAACACGCA | 1080 |
| Seq_1 | 1081 | TATCTTTACTTCCAAGAACCCAGTTCAATTGCCGTGACTGCCCTACCAAGTACCGAGAT | td69 |
| Seq_2 | 1081 | TATCTTTACTTCCAAGAACCCAGTTCAATTGCCGTGACTGCCCTACCAAGTACCGAGAT | td70 |
| Seq_1 | 1141 | TACTCAGCTGAAATTGATAATAACCCCTTGCCAAAGGATTCCGGAGAACCTTGAGTC | 1200 |
| Seq_2 | 1141 | TACTCAGCTGAAATTGATAATAACCCCTTGCCAAAGGATTCCGGAGAACCTTGAGTC | 1200 |
| Seq_1 | 1201 | CATGTACACATCTGTTGACACCAGCATCCCCCTCCCGCCTGGACCAACTGTCAATTCC | 1260 |
| Seq_2 | 1201 | CATGTACACATCTGTTGACACCAGCATCCCCCTCCCGCCTGGACCAACTGTCAATTCC | 1260 |
| Seq_1 | 1261 | TGGGGGAGATCACTACTCTCCTCTCCCTACCCAAACCGAGTATCCTGTTCCCGCCCTTA | 1320 |
| Seq_2 | 1261 | TGGGGGAGATCACTACTCTCCTCTCCCTACCCAAACCGAGTATCCTGTTCCCGCCCTTA | 1320 |
| Seq_1 | 1321 | CCCCGACCTTCTGGCCAGGGCAAGGATGTGGTCCCCCAGGCTTACTGGCTGGGGCCCC | 1380 |
| Seq_2 | 1321 | CCCCGACCTTCTGGCCAGGGCAAGGATGTGGTCCCCCAGGCTTACTGGCTGGGGCCCC | 1380 |
| Seq_1 | 1381 | CCGGGACCACTATGGCTGAGTTGAGCAGTCAGCATGAAGCCTGCATTCTGCC | 1440 |
| Seq_2 | 1381 | CCGGGACCACTATGGCTGAGTTGAGCAGTCAGCATGAAGCCTGCATTCTGCC | 1440 |

Fig. 8 Cont.

| | | | |
|-------|------|---|------|
| Seq_1 | 1441 | CTCTGCCCTGGGCCCACCATGTCTACTACCGAGGCCAGGAGGTCTGGCACCTGGAGC | 1500 |
| Seq_2 | 1441 | CTCTGCCCTGGGCCCACCATGTCTACTACCGAGGCCAGGAGGTCTGGCACCTGGAGC | 1500 |
| Seq_1 | 1501 | TGGCTGGCTGTGGCACCCAGTACCCCTCCAAGATGGGCCGGCCAGCTGGTTCGCC | 1560 |
| Seq_2 | 1501 | TGGCTGGCTGTGGCACCCAGTACCCCTCCAAGATGGGCCGGCCAGCTGGTTCGCC | 1560 |
| Seq_1 | 1561 | TATGCGGACTCTGCCCATGGAACCCGGCCCTGGAGGCTCAGAGGGACGGGACAGAGGA | 1620 |
| Seq_2 | 1561 | TATGCGGACTCTGCCCATGGAACCCGGCCCTGGAGGCTCAGAGGGACGGGACAGAGGA | 1620 |
| Seq_1 | 1621 | CCAGGGTCCCCCTGGGTGTGGACTGAGATTGCCCATCGCCGGAAATCCAGTGAATTC | 1680 |
| Seq_2 | 1621 | CCAGGGTCCCCCTGGGTGTGGACTGAGATTGCCCATCGCCGGAAATCCAGTGAATTC | 1680 |
| Seq_1 | 1681 | AGGACTGGCGAAGGAGACTCTAACAGAGGAGCGCGTGTCCCCCTATCCTTCAGTGGTGA | 1740 |
| Seq_2 | 1681 | AGGACTGGCGAAGGAGACTCTAACAGAGGAGCGCGTGTCCCCCTATCCTTCAGTGGTGA | 1740 |
| Seq_1 | 1741 | CAGCTCCTCCCTGCTGGGCCCTTCCTCCCTTGTATAAGGAAGCTGAAGGACAGTTTA | 1800 |
| Seq_2 | 1741 | CAGCTCCTCCCTGCTGGGCCCTTCCTCCCTTGTATAAGGAAGCTGAAGGACAGTTTA | 1800 |
| Seq_1 | 1801 | TAACTATTTCCAACGTGAGCAGATGACATGATGAAAGGAACAGAAACAGTGTATTAGG | 1860 |
| Seq_2 | 1801 | TAACTATTTCCAACGTGAGCAGATGACATGATGAAAGGAACAGAAACAGTGTATTAGG | 1860 |
| Seq_1 | 1861 | TTGGAGGACACCGACTAATTGGGAAACGGATGAAGGACTGAGAAGGCCCGCTCCCTC | 1920 |
| Seq_2 | 1861 | TTGGAGGACACCGACTAATTGGGAAACGGATGAAGGACTGAGAAGGCCCGCTCCCTC | 1920 |
| Seq_1 | 1921 | TGGCCCTCTGTGTTAGTAGTTGGTGGGAAGTGGGCTCAAGAAGGATTTGGGTT | 1980 |
| Seq_2 | 1921 | TGGCCCTCTGTGTTAGTAGTTGGTGGGAAGTGGGCTCAAGAAGGATTTGGGTT | 1980 |
| Seq_1 | 1981 | CACCAAGATGCTTCCTGGCCACGATGAAACCTGAGAGGGGTGTCCCCCTGCCCATCCTC | 2040 |
| Seq_2 | 1981 | CACCAAGATGCTTCCTGGCCACGATGAAACCTGAGAGGGGTGTCCCCCTGCCCATCCTC | 2040 |
| Seq_1 | 2041 | TGCCCTAACTACAGTCGTTACCTGGTGTGCGTCTGCTTTGGTTCCAGCTGGAGAA | 2100 |
| Seq_2 | 2041 | TGCCCTAACTACAGTCGTTACCTGGTGTGCGTCTGCTTTGGTTCCAGCTGGAGAA | 2100 |
| Seq_1 | 2101 | AAGAAGACAAGAAAGTCTTGGCATGAAGGAGCTTTTGCACTAGTAGGGTGGGAGGGT | 2160 |
| Seq_2 | 2101 | AAGAAGACAAGAAAGTCTTGGCATGAAGGAGCTTTTGCACTAGTAGGGTGGGAGGGT | 2160 |
| Seq_1 | 2161 | CAGGTGTGGACATGGGAGCAGGAGACTCCACTTCTCCTTGTACAGTAACCTTCAAC | 2220 |
| Seq_2 | 2161 | CAGGTGTGGACATGGGAGCAGGAGACTCCACTTCTCCTTGTACAGTAACCTTCAAC | 2220 |
| Seq_1 | 2221 | CTTTCTGTTGGCATGTGTTAACCTCTGATCCAAAAGAACAAATACAGTATGTTATA | 2280 |
| Seq_2 | 2221 | CTTTCTGTTGGCATGTGTTAACCTCTGATCCAAAAGAACAAATACAGTATGTTATA | 2280 |
| Seq_1 | 2281 | ACCATCAGCCCCCAGGGTCAGGAAAGGACTCACCTGACTTGGACAGCTGGCTGGC | 2340 |
| Seq_2 | 2281 | ACCATCAGCCCCCAGGGTCAGGAAAGGACTCACCTGACTTGGACAGCTGGCTGGC | 2340 |
| Seq_1 | 2341 | TCCCCCTGCTCAAACACAGTGGGATCAGAGAAAAGGGCTGGAAAGGGGGATGGCCC | 2400 |
| Seq_2 | 2341 | TCCCCCTGCTCAAACACAGTGGGATCAGAGAAAAGGGCTGGAAAGGGGGATGGCCC | 2400 |
| Seq_1 | 2401 | ACATCTCAAGAACAGATATTGTTGGTGTGTTGGTGTGTGTTTTCTT | 2460 |
| Seq_2 | 2401 | ACATCTCAAGAACAGATATTGTTGGTGTGTTGGTGTGTGTTG----- | 2450 |
| Seq_1 | 2461 | TTCTTCTTTTATTGGGGAGGCTATTATGACTGAGAGTGGTGTCT | 2520 |
| Seq_2 | **** | ----- | **** |
| Seq_1 | 2521 | GGATATATTCTTTGTCTCATCACTTCTGAAAATAACATAAAACTGTAAAAAAA | 2580 |
| Seq_2 | **** | ----- | **** |
| Seq_1 | 2581 | AAAAAAA | 2589 |
| Seq_2 | **** | ----- | **** |

CGGCCCCGCTGGAGAGGAAGCCCGAGAGCTGCCGCCCTGCCGGACGAG
 GGCCTAGAACGCCAGCGTCAGAGCCGGCTCGGGTCCCCCACCC
 GGCCTCGGGTCCCCGCCCTGCTCCCTGCCATCCCAGCCCACGCGA
 CCCCTCGCGCGGGAGGGGGCTCGACGGTACGGGAAGGTGCCA
 GCCCAGGGATGGGCATCGTGAGCCGGGTTGCCAGACATGCTGACG
 GGCACCGAGCCGATGCCGGGAGCGACGAGGGCCGGCGCTGGCGCGA
 CCCGCAGCACCGTACTTCTACCCGGAGCCGGCGCAGGACGGGACG
 AGCGTCGGGGGGCGGCAGCCTGGGTCTCCCTACCCGGGGGGCGCTTG
 GTGCCCGCCCCGCCAGCGCTTCCTGGAGCTACGCCAACCGGCCG
 ACCCCAGCGGCCGGCTTCCCGGCCGCGGGAGTCCTCCGCCGCGCG
 CGGACGCCGAGGGCTACCGCCGGCGAGGGCTACGCCGCCCGGACCG
 CGGCCGGGCTTACCCGGGGCGGTGAGGACTACGCCAACCGGCCG
 ACTGGAGGTGCGGGAAACTGAGGGTGCCTCAACAAACACCTGTTGT
 GGTCCAAGTTAACGACCAAGAGATGATCATACCAAGCAGGGA
 CGGGGATGTTCCCATTCCTGTCATTACTGTGCCGGCTGGAGCCAC
 CAGCCACTACAGGGATGTTGTGGACGTGGCTTGGGACAGCACCAC
 GCGGTACCAAGCGGCAAGTGGTGCAGTGTGGAAAGGCCGAGGGCAGC
 ATGCCAGGAAACCGCTGTACGCCACCCGGACTCCCCAACACAGGAGC
 GCACTGGATGCCAGGAAGTTTCAATTGGAAACTAAAGCTACAAACA
 ACAAGGGGGCGTCAACAATGTGACCCAGATGATTGTGCTCCAGTCCCTC
 CATAAGTACCAAGCCCCGGCTGCATATCGTGGAGGTGAACGACGGAGAGCC
 AGAGGCAGCTGCAACGCTTCAACACGCATATTTACTTTCCAAGAAA
 CCCAGTCATTGGCGTGAUTGCCCTACCAAGATGCCGAGATTACTCAGTG
 AAAATTGATAATAACCCCTTGCCAAAGGATTCCGGGAGAACTTTGAGTC
 CAGAACACCTGACACCGAGCTCCCTCCCCGCCCTGGACCAACT
 CCAATTCCCTGGGGAGCACTACTCTCCCTCCCTACCCAAACCA
 CCTTCTCCAGCCGCTTCAACCCGACCTTCTGGCAGGGAGGAGG
 GCTCCCAAGGCTACTGGCTGGGGCCCCCGGACACAGCTGGAGG
 CTGAGTTTCGAGCAAGCGAGACGGCTGCTTGGCCCTCTGCCCCCT
 GGGCCCAACCGCTTCAACACGCATATTTACTTTCCAAGAAA
 TGGCTGGCCTGGCAGCCCAACTACCCCTCCCAAGGGGGCCAGCT
 GCTCCGCCCCGCGGACTCTGCCCTGGGGCCCTGGAGGCTCA
 GAGGGACGGGACAGAGGACCAAGGCTCCCTTGCTGGAGGAG
 TGCCCCCTCCGGGGAGCAACGCTTCAACACGCATATTTACTTTCCAAGAAA
 CTAAGAGGAGGCGCTTACCCCTTCTTCAAGGAGCTGAAGGACA
 CCTGCTGGGGCCCTTCTCTTCAAGGAGCTGAAGGACA
 TAACATTTCCTCAACTGAGCAGGACAGCTGGGAAACCGGAGAAGGACT
 GAGAAGGCCCCCGCTCCCTTCTGGCCCTCTCTTCAAGGAGCTGA
 GAAAGGGCTCAAGAAGGCTTGGGCTTCAACCAAGGAGCTTTC
 ACGGAAACCTGAGAGGCTCCCTTGCTGCCCTCCTGCCCC
 ACACCTTACCTGCTGCTGCTTCTGGCTTTGCTTCAAGCTGGAGAA
 AAGAAGACAAGAAAACCTGGGCTGAAGGAGCTTTGCTTCAAGG
 GGGAGGGCAGGGGACAGGGGAGCAGGAGACTCCACTTCTTCC
 TTTACACAACTTCAACCTTTGCTTGGCTTCAAGGAGCTTCA
 CCAAAAGAACAAACACGAAACCTGGGAGCTTCAAGGAGCT
 AGGGAAAGGACTCACCTGACTTGGACAGCTGGCTGGGCTCCCCCTGCT
 CAAACACAGGGGAGAGGAGAAAGGGGCTGGAAAGGGGGAAAGGCC
 ACACCTCAAGAACGAGGAGCTTCAAGGAGCTGGCTGGGCTGGG
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 TGAAAACAAACAAACAGTAAACAAAAAA

Fig. 8A

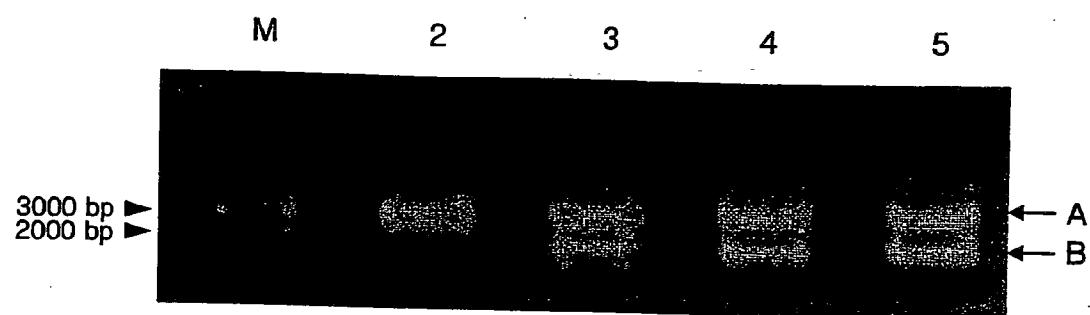


Fig. 9

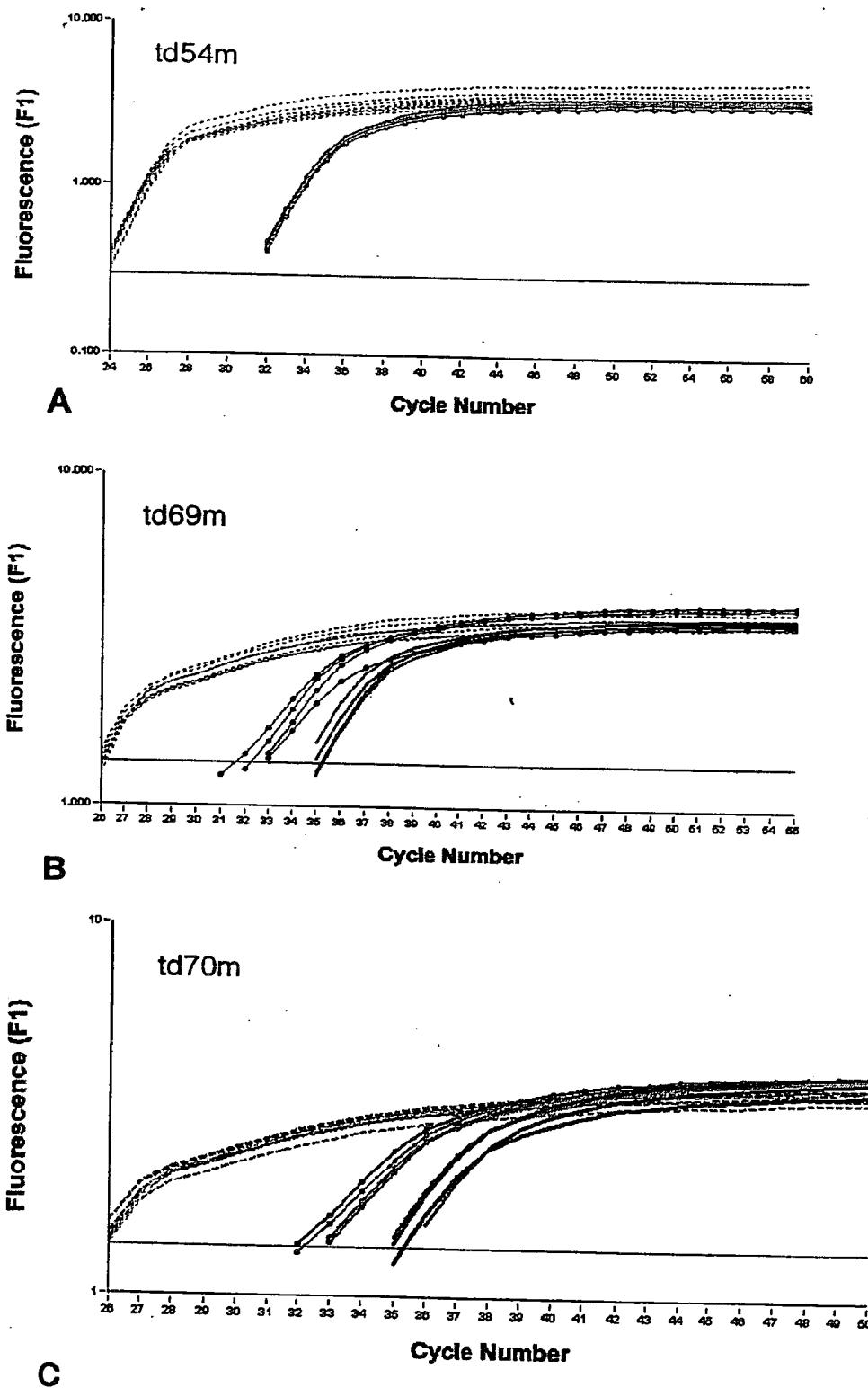


Fig. 10

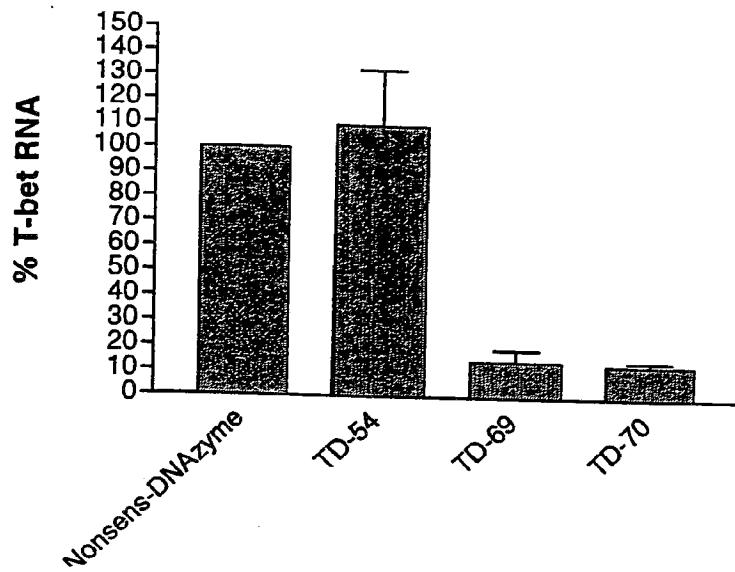


Fig. 11